STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _10/551,977A_

Source: _1 Fwlib_

Date Processed by STIC: _7/18/07_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER
VERSION 4.4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> **http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission
   User Manual** - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: *10/551,977A*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
   Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
   prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
   Numbering   use space characters, instead.

4 ____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
   ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,**
   each n or Xaa can only represent a single residue. Please present the maximum number of each
   residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
   "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
   previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
   the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for**
   Artificial or Unknown sequences.

7 ____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
   (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   This sequence is intentionally skipped
   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
   (NEW RULES)   <210> sequence id number
   <400> sequence id number
   000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
   (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
   Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
   is Artificial Sequence. (see item 11 below)

11 ____ Use of <220>   Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use
   of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
   Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
   explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
   Sequence Rules

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
   "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
   listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – STIC Systems Branch – 03/02/06

IFW16

RAW SEQUENCE LISTING   DATE: 01/18/2007
PATENT APPLICATION: US/10/551,977A   TIME: 10:42:16

Input Set : A:\SeqList.txt
Output Set: N:\CRF4\01182007\J551977A.raw

```
 4 <110> APPLICANT: DEPERTHES, David
 5         CLOUTIER, Sylvain
 6         MACH, Jean-Pierre
 7         HOLLER, Nils
 8         FATTAH, Omar
10 <120> TITLE OF INVENTION: PEPTABODY FOR CANCER TREATMENT
12 <130> FILE REFERENCE: KZI-002US
14 <140> CURRENT APPLICATION NUMBER: 10/551977A
15 <141> CURRENT FILING DATE: 2005-10-04
17 <150> PRIOR APPLICATION NUMBER: PCT/IB2004/001049
18 <151> PRIOR FILING DATE: 2004-04-05
20 <150> PRIOR APPLICATION NUMBER: US 60/460,490
21 <151> PRIOR FILING DATE: 2003-04-04
23 <160> NUMBER OF SEQ ID NOS: 30
25 <170> SOFTWARE: PatentIn version 3.1
```

see pp. 1-2

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
131 <210> SEQ ID NO: 6
132 <211> LENGTH: 6        delete - this is not a DNA sequence
133 <212> TYPE: DNA
134 <212> TYPE: PRT
135 <213> ORGANISM: Artificial sequence
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Enhancer Peptide
140 <400> SEQUENCE: 6
141 Tyr Ser Phe Glu Asp Leu
E--> 142 1           5       5 ← misaligned amino acid number (see item 3 on Error Summary Sheet)
144 <210> SEQ ID NO: 7
145 <211> LENGTH: 7
146 <212> TYPE: PRT
147 <213> ORGANISM: Artificial sequence
149 <220> FEATURE:
150 <223> OTHER INFORMATION: Enhancer Peptide
152 <400> SEQUENCE: 7
153 Tyr Ser Phe Glu Asp Leu Tyr
E--> 154 1           5       5 ← same error
156 <210> SEQ ID NO: 8
157 <211> LENGTH: 8
158 <212> TYPE: PRT
159 <213> ORGANISM: Artificial sequence
161 <220> FEATURE:
```

```
     162 <223> OTHER INFORMATION: Enhancer Peptide
     164 <400> SEQUENCE: 8
     165 Tyr Ser Phe Glu Asp Leu Tyr Arg
E--> 166 1            5        5 ← same error
     168 <210> SEQ ID NO: 9
     169 <211> LENGTH: 9
     170 <212> TYPE: PRT
     171 <213> ORGANISM: Artificial sequence
     173 <220> FEATURE:
     174 <223> OTHER INFORMATION: Enhancer Peptide
     176 <400> SEQUENCE: 9
     177 Tyr Ser Phe Glu Asp Leu Tyr Arg Arg
E--> 178 1            5        5 ←
     191 <210> SEQ ID NO: 11
     192 <211> LENGTH: 25
     193 <212> TYPE: PRT
     194 <213> ORGANISM: Spodoptera litura
     196 <400> SEQUENCE: 11
     197 Glu Asn Phe Ser Gly Gly Cys Val Ala Gly Tyr Met Arg Thr Pro Asp
     198 1                5                10              15
     199 Gly Arg Cys Lys Pro Thr Phe Tyr Gln
E--> 200 20 25        20              25 ←
```

VERIFICATION SUMMARY   DATE: 01/18/2007
PATENT APPLICATION: **US/10/551,977A**   TIME: 10:42:17

Input Set : **A:\SeqList.txt**
Output Set: **N:\CRF4\01182007\J551977A.raw**

```
L:102 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:100
L:134 M:280 W: Numeric Identifier already exists, Type not replaced.
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:142 M:301 E: (44) No Sequence Data was Shown, SEQ ID:6
L:142 M:252 E: No. of Seq. differs, <211> LENGTH:Input:6 Found:0 SEQ:6
L:154 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:166 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:178 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:200 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
```